

## SEQUENCE LISTING

<110> LUKYANOV, Sergei Anatolievich  
SHAGIN, Dmitry Alexeevich  
YANUSHEVICH, Yury Grigorievich

<120> FLUORESCENT PROTEINS AND CHROMOPROTEINS FROM NON-AEQUOREA HYDROZOA  
SPECIES AND METHODS FOR USING SAME

<130> XXX

<160> 22

<170> PatentIn version 3.1

<210> 1

<211> 784

<212> DNA

<213> Phialidium sp.

<400> 1

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gtaccagttc catggtcaac tttagtaaca acacttactt atggtgcaca atgcttcgcc	240
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gatcacaggg ataacatgag cttggttgaa accgtacggg ctgtggattg cagaaaaaca	720
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<210> 2

<211> 234

<212> PRT

<213> Phialidium sp.

<400> 2

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Glu	Met	Glu	Gly	Asn	Val	Asp	Gly	His	Thr	Phe	Ser	Ile	Arg	Gly	Lys
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<210> 3
<211> 705
<212> DNA
<213> Artificial sequence
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<223> phiYFP-Y1 mutant sequence
<400> 3
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<212> PRT
<213> Artificial sequence
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<223> phiYFP-Y1 mutant sequence
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Glu	Met	Glu	Gly	Asn	Val	Asp	Gly	His	Thr	Phe	Ser	Ile	Arg	Gly	Lys
			20					25					30		
Gly	Tyr	Gly	Asp	Ala	Ser	Val	Gly	Lys	Val	Asp	Ala	Gln	Phe	Ile	Cys
		35					40					45			
Thr	Thr	Gly	Asp	Val	Pro	Val	Pro	Trp	Ser	Thr	Leu	Val	Thr	Thr	Leu
	50					55					60				
Thr	Tyr	Gly	Ala	Gln	Cys	Phe	Ala	Lys	Tyr	Gly	Pro	Glu	Leu	Lys	Asp
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**IPEA/RU**  
**AMENDED SHEET**

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<212> PRT
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<400> 6
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**IPEA/RU**  
**UNLEADED STREET**

19 May 2004

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 50 55 60  
 Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp  
 65 70 75 80  
 Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile  
 85 90 95  
 Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe  
 100 105 110  
 Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe  
 115 120 125  
 Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr  
 130 135 140  
 Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys  
 145 150 155 160  
 Ser Ala Phe Lys Ile Arg His Glu Ile Thr Gly Ser Lys Gly Asp Phe  
 165 170 175  
 Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro  
 180 185 190  
 Val His Val Pro Glu Asn His His Met Ser Tyr His Val Lys Leu Ser  
 195 200 205  
 Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val  
 210 215 220  
 Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu  
 225 230

&lt;210&gt; 7

&lt;211&gt; 705

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; phiYFP-M1 mutant sequence

&lt;400&gt; 7

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aaagttgatg	cccaattcat	ctgcacaact	ggagatgtac	cagttccatg	gtcaacttta	180
gtaacaacac	ttacttatgg	tgcacaatgc	ttcgccaaat	atggtccaga	attaaaggat	240
ttctacaaga	gttgcatgcc	tgatggctat	gtgcaggagc	gtacaatcac	atttgaagg	300
gacggaaact	ttaaaactcg	cgctgaagtt	acatttgaaa	acggatctgt	ttataaccga	360
gtcaaaactta	atggacaagg	atttaagaaa	gacggacatg	tgcttggaag	gaatcttgaa	420
ttcaatttca	cacctcattg	tctttacatt	tggggagatc	aggctaata	tggtttgaag	480
tctgctttca	aaatttgcca	tgagattact	ggatcaaaaag	gagacttcat	tgttgcagac	540
cacacccaaa	tgaacacacc	cattggtggt	ggaccagtcc	atgtccctga	ataccatcat	600
atgagctacc	atgtcaagct	cagcaaagat	gttactgatc	acagggataa	catgagcttg	660
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&lt;210&gt; 8

&lt;211&gt; 234

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; phiYFP-M1 mutant sequence

&lt;400&gt; 8

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu  
 50 55 60  
 Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp  
 65 70 75 80  
 Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile  
 85 90 95  
 Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe  
 100 105 110  
 Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe  
 115 120 125  
 Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr  
 130 135 140  
 Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys  
 145 150 155 160  
 Ser Ala Phe Lys Ile Arg His Glu Ile Thr Gly Ser Lys Gly Asp Phe  
 165 170 175  
 Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro  
 180 185 190  
 Val His Val Pro Glu Asn His His Met Ser Tyr His Val Lys Leu Ser  
 195 200 205  
 Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val  
 210 215 220  
 Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu  
 225 230

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 <212> DNA  
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 aaagttgatg cccaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta 180  
 gtaacaacac ttacttatgg tgcacaatgc ttcgccaaat atggtccaga attaaaggat 240  
 ttctacaaga gttgcatgcc tgatggctat gtgcaggagc gtacaatcac atttgaaggg 300  
 gacggaaact ttaaaactcg cgctgaagtt acatttgaaa acggatctgt ttataaccga 360  
 gtcaaactta atggacaagg atttaagaaa gacggacatg tgcttggaag gaatcttgaa 420  
 ttcaatttca cacctcattg tctttacatt tggggagatc aggctaataca tgggttgaag 480

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tctgctttca aaatttgcca tgagattact ggatcaaaag gagacttcat tgttgagac 540
cacacccaaa tgaacacacc cattggtggt ggaccagtcc atgtccctga ataccatcat 600
atgagctacc atgtcaagct cagcaaagat gttactgatac acagggataa catgagcttg 660
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<210> 8
<211> 234
<212> PRT
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<400> 8

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Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1           5           10           15
Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20           25           30
Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35           40           45
Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50           55           60
Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65           70           75           80
Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
85           90           95
Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
100          105          110
Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115          120          125
Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130          135          140
Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145          150          155          160
Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
165          170          175
Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
180          185          190
Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser
195          200          205
Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
210          215          220

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Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu  
225 230

<210> 9  
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<400> 9

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aaggtggatg cccagttcat ctgcaccacc ggcgatgtgc ccgtgccctg gagcaccctg      180
gtgaccaccc tgacctacgg cgcccagtgct ttcgccaaagt acggccccga gctgaaggat      240
ttctacaaga gctgcatgcc cgatgggtac gtgcaggagc gcaccatcac cttcgagggc      300
gatggcaatt tcaagaccgg cgccgaggtg accttcgaga atggcagcgt gtacaatcgc      360
gtgaagctga atggccaggg cttcaagaag gatggccacg tgctgggcaa gaatctggag      420
ttcaatttca cccccactg cctgtacatc tggggcgatc aggccaatca cggcctgaag      480
agcgccttca agatctgcca cgagatcacc ggcagcaagg gcgatttcat cgtggccgat      540
cacaccaga tgaatacccc catcggcggc ggccccgtgc acgtgcccga gtaccaccac      600
atgagctacc acgtgaagct gagcaaggat gtgaccgatc accgcgataa tatgagcctg      660
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<210> 10  
<211> 234  
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<400> 10

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1          5          10          15
Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
          20          25          30
Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
          35          40          45
Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
          50          55          60
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Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp  
 65 70 75 80  
 Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile  
 85 90 95  
 Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe  
 100 105 110  
 Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe  
 115 120 125  
 Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr  
 130 135 140  
 Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys  
 145 150 155 160  
 Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe  
 165 170 175  
 Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro  
 180 185 190  
 Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser  
 195 200 205  
 Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val  
 210 215 220  
 Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu  
 225 230

&lt;210&gt; 11

&lt;211&gt; 1047

&lt;212&gt; DNA

&lt;213&gt; hydromedusa 1 from sub-order Anthomedusae

&lt;400&gt; 11

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 ggtgtcaaaa atttacgttc tagaaattgc agtacggaag aaaaacccgt cataacttgg 180  
 gcaatgacag aaacatttca gaaaaaattg ccatataagt tagaattgga tggagatggt 240  
 gatgggcaaa catttaaggt tattggtgag ggcgttgagg atgcaaccac tgggtgaatt 300  
 gaaggaaaat atgtttgtac agaaggagaa gttcctatct catgggtttc gctcatcacc 360  
 tcattaagtt atggtgcgaa atgttttggt cgatatccaa atgaaataaa tgattttttc 420  
 aaaagtactt ttccttctgg atatcatcaa gaaagaaaaa ttacatatga gaatgatggt 480  
 gtttttagaaa cagcagctaa aattactatg gaaagtgggt caatagtga tagaataaat 540  
 gtgaaaggca caggcttcga taaagatggt catgtatgcc aaaaaaatct tgaatcctcc 600  
 cctccttcga caacatatgt tggtcccgag ggagaaggta ttcgaatcat ctatagaaac 660  
 atctatccaa caaagatgg tcactatggt gttgccgaca cacagcaagt aaatcgacca 720



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attagagcac aaggaacatc agctatccca acatatcatc acattaaatc gaaagttgat      780
ctttcaacag atccagaaga aaataaagat catattatca tcaaagaaac caactgcgca      840
tttgacgctg atttttctta agatttccga ttgcatcaa gattgaaaaa ctaaataaag      900
ataggtaaaa aaaatatgtc ttgatgttta catacagtat tgatataagc ttcaaagaaa      960
tatattttca aataaaacttt ataaaattag gaatctttga atatataaac taaacctttt     1020
atttgtagaa taaaaataat taaagac                                           1047

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&lt;210&gt; 12

&lt;211&gt; 262

&lt;212&gt; PRT

&lt;213&gt; hydromedusa 1 from sub-order Anthomedusae

&lt;400&gt; 12

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Met Asn Val Met Arg Tyr Asn Arg Gly Phe Cys Arg Val Leu Gln Asn
1           5           10           15
Gly Val Lys Asn Leu Arg Ser Arg Asn Cys Ser Thr Glu Glu Lys Pro
          20           25           30
Val Ile Leu Gly Ala Met Thr Glu Thr Phe Gln Lys Lys Leu Pro Tyr
          35           40           45
Lys Leu Glu Leu Asp Gly Asp Val Asp Gly Gln Thr Phe Lys Val Ile
          50           55           60
Gly Glu Gly Val Gly Asp Ala Thr Thr Gly Val Ile Glu Gly Lys Tyr
65           70           75           80
Val Cys Thr Glu Gly Glu Val Pro Ile Ser Trp Val Ser Leu Ile Thr
          85           90           95
Ser Leu Ser Tyr Gly Ala Lys Cys Phe Val Arg Tyr Pro Asn Glu Ile
          100          105          110
Asn Asp Phe Phe Lys Ser Thr Phe Pro Ser Gly Tyr His Gln Glu Arg
          115          120          125
Lys Ile Thr Tyr Glu Asn Asp Gly Val Leu Glu Thr Ala Ala Lys Ile
          130          135          140
Thr Met Glu Ser Gly Ala Ile Val Asn Arg Ile Asn Val Lys Gly Thr
145          150          155          160
Gly Phe Asp Lys Asp Gly His Val Cys Gln Lys Asn Leu Glu Ser Ser
          165          170          175
Pro Pro Ser Thr Thr Tyr Val Val Pro Glu Gly Glu Gly Ile Arg Ile
          180          185          190
Ile Tyr Arg Asn Ile Tyr Pro Thr Lys Asp Gly His Tyr Val Val Ala
          195          200          205
Asp Thr Gln Gln Val Asn Arg Pro Ile Arg Ala Gln Gly Thr Ser Ala
210          215          220

```

Ile Pro Thr Tyr His His Ile Lys Ser Lys Val Asp Leu Ser Thr Asp  
 225                                      230                                      235                                      240  
 Pro Glu Glu Asn Lys Asp His Ile Ile Ile Lys Glu Thr Asn Cys Ala  
    245                                      250                                      255  
 Phe Asp Ala Asp Phe Ser  
    260

<210> 13  
 <211> 1089  
 <212> DNA  
 <213> hydromedusa 2 from sub-order Anthomedusae  
 <400> 13

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cattatttca atccgatatg acattcaaga tcttcatcga tggagtgggtg aatgatcaga      180
aattcacgat aatcgcagat ggatcgctcca aattcccca tggtgacttc aacgtgcatg      240
ctgtgtgcga aaccgggaaa ctcccaatgt catggaaacc tatttgtcac cttatccaat      300
acggggagcc attctttgca aaatatccca atggcatcag ccattttgca caggagtgtc      360
ttccagaagg attaacaatt gatcgaacag tcagattcga aaatgacggc actatgacgt      420
ctcaccacac ctatgagttg gacggcacct gtgtcatttc caggataacc gttaattgtg      480
acggatttca acctgatgga ccaatcatga aagaccagct tgttgatatc ctgccaactg      540
agacacatat gttccctcat gggccaatg ctgtcagaca attgtgttac attggcttca      600
cgacagctga tgggtgtctc atgatgtcac attttgattc gaaattgaca ttcaatggtt      660
cgagagcaat caagattcct ggacctcatt tcgttactgt gataatcaaa cagatgaaag      720
atacaagcga caagcgtgat catgtgtgtc aacgtgaagt cacctacgct cactcagttc      780
cacgcatcac ttctgctatc taaacatcat tcttaaaagg ggaacatgca catcatactt      840
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tcgttttagat gttgaaggac gaaatgacgac aaagagatta atagagactc atatttttat      960
gtagaatcga ttcattcagc ccattggtaa cctttttggt attttatcat cttattattg     1020
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aagaacttg                                     1089
  
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<210> 14  
 <211> 232  
 <212> PRT  
 <213> hydromedusa 2 from sub-order Anthomedusae  
 <400> 14

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 1                                      5                                      10                                      15

Phe Ile Asp Gly Val Val Asn Asp Gln Lys Phe Thr Ile Ile Ala Asp  
 20 25 30  
 Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys  
 35 40 45  
 Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile  
 50 55 60  
 Gln Tyr Gly Glu Pro Phe Phe Ala Lys Tyr Pro Asn Gly Ile Ser His  
 65 70 75 80  
 Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Thr Ile Asp Arg Thr Val  
 85 90 95  
 Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu  
 100 105 110  
 Asp Gly Thr Cys Val Ile Ser Arg Ile Thr Val Asn Cys Asp Gly Phe  
 115 120 125  
 Gln Pro Asp Gly Pro Ile Met Lys Asp Gln Leu Val Asp Ile Leu Pro  
 130 135 140  
 Thr Glu Thr His Met Phe Pro His Gly Ser Asn Ala Val Arg Gln Leu  
 145 150 155 160  
 Cys Tyr Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His  
 165 170 175  
 Phe Asp Ser Lys Leu Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro  
 180 185 190  
 Gly Pro His Phe Val Thr Val Ile Ile Lys Gln Met Lys Asp Thr Ser  
 195 200 205  
 Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser  
 210 215 220  
 Val Pro Arg Ile Thr Ser Ala Ile  
 225 230

&lt;210&gt; 15

&lt;211&gt; 699

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; S3-2 mutant of the hm2CP

&lt;400&gt; 15

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 gacttcaacg tacatgctgt gtgcgaaacc gggaaactcc caatgtcatg gaaaccatt 180  
 tgtcacctta tccaatacgg ggagccattc ttgcaagat atcccaacgg catcagccat 240

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tttgcacagg agtgctttcc agaaggatta tcaattgatc gaacagtcag attcgaaaat    300
gacggcacta tgacgtctca ccacacctat gagttggacg gcacctgtgt cgtttccagg    360
ataaccgtta attgtgacgg atttcaacct gatggaccaa tcatgagaga ccagcttggt    420
gatatcctgc caaacgagac acatatgttc cctcatggac ccaatgctgt cagacaattg    480
gctttcatag gcttcacgac agctgatggg ggtctcatga tgtcacattt tgattcgaaa    540
atgacattca atggttcgag agcaatcaag attcctggac ctcatttcgt cactaccata    600
accaaacaga tgaaagatac aagcgacaag cgtgatcatg tgtgtcagcg ggaagtcacc    660
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<210> 16

<211> 232

<212> PRT

<213> Artificial sequence

<220>

<223> S3-2 mutant of the hm2CP

<400> 16

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Met Glu Gly Gly Pro Ala Leu Phe Gln Ser Asp Met Thr Phe Lys Ile
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Phe Ile Asp Gly Val Val Asn Gly Gln Lys Phe Thr Ile Val Ala Asp
              20              25              30
Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys
              35              40              45
Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile
              50              55              60
Gln Tyr Gly Glu Pro Phe Phe Ala Arg Tyr Pro Asn Gly Ile Ser His
65              70              75              80
Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Ser Ile Asp Arg Thr Val
              85              90              95
Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu
              100             105             110
Asp Gly Thr Cys Val Val Ser Arg Ile Thr Val Asn Cys Asp Gly Phe
              115             120             125
Gln Pro Asp Gly Pro Ile Met Arg Asp Gln Leu Val Asp Ile Leu Pro
              130             135             140
Asn Glu Thr His Met Phe Pro His Gly Pro Asn Ala Val Arg Gln Leu
145             150             155             160
Ala Phe Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His
              165             170             175
Phe Asp Ser Lys Met Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro
              180             185             190

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Gly Pro His Phe Val Thr Thr Ile Thr Lys Gln Met Lys Asp Thr Ser  
 195 200 205  
 Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser  
 210 215 220  
 Val Pro Arg Ile Thr Ser Ala Ile  
 225 230

<210> 17  
 <211> 705  
 <212> DNA  
 <213> Artificial sequence  
 <220>  
 <223> phiYFP-MlG1 mutant, derived from humanized version of the phiYFP-M1  
 M1  
 <400> 17

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 aatgtggatg gccacacctt cagcatccgc ggcaagggt acggcgatgc cagcgtgggc 120  
 aaggtggatg ccagttcat ctgcaccacc ggcgatgtgc ccgtgccctg gagcaccctg 180  
 gtgaccaccc tgtcctacgg cgcccagtgc ttcgccaagt acggccccga gctgaaggat 240  
 ttctacaaga gctgcatgcc cgatggctac gtgcaggagc gcaccatcac cttcgagggc 300  
 gatggcaatt tcaagacccg cgccgaggtg accttcgaga atggcagcgt gtacaatcgc 360  
 gtgaagctga atggccaggg cttcaagaag gatggccacg tgctgggcaa gaatctggag 420  
 ttcaatttca cccccactg ccagtacatc tggggcgatc aggccaatca cggcctgaag 480  
 agcgccttca agatctgcca cgagatcacc ggcagcaagg gcgatttcat cgtggccgat 540  
 cacaccaga tgaatacccc catcggcggc ggccccgtgc acgtgcccga gtaccaccac 600  
 atgagcaccc acgtgaagct gagcaaggat gtgaccgatc accgcgataa tatgagcctg 660  
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<210> 18  
 <211> 234  
 <212> PRT  
 <213> Artificial sequence  
 <220>  
 <223> phiYFP-MlG1 mutant, derived from humanized version of the phiYFP-M1  
 M1  
 <400> 18

Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val  
 1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys  
                   20                                  25                                  30  
 Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys  
                   35                                  40                                  45  
 Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu  
                   50                                  55                                  60  
 Ser Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp  
 65                                  70                                  75                                  80  
 Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile  
                                   85                                  90                                  95  
 Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe  
                   100                                  105                                  110  
 Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe  
                   115                                  120                                  125  
 Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr  
                   130                                  135                                  140  
 Pro His Cys Gln Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys  
 145                                  150                                  155                                  160  
 Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe  
                                   165                                  170                                  175  
 Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro  
                   180                                  185                                  190  
 Val His Val Pro Glu Tyr His His Met Ser Thr His Val Lys Leu Ser  
                   195                                  200                                  205  
 Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val  
                   210                                  215                                  220  
 Arg Ala Val Asp Cys Arg Thr Ala Tyr Leu  
 225                                  230

&lt;210&gt; 19

&lt;211&gt; 705

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

<223> phiYFP-M1C1 mutant, derived from humanized version of the phiYFP-  
 M1

&lt;400&gt; 19

atgtccagcg gcgcccagct gttccacggc aagatcccct acgtggtgga gatggagggc 60  
 aatgtggatg gccacacctt cagcatccgc ggcaagggct acggcgatgc cagcgtgggc 120  
 aaggtggatg ccagttcat ctgcaccacc ggcgatgtgc ccgtgccctg gagcaccctg 180

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gtgaccaccc tgtcctgggg cgcccagtcg ttcgccaagt acggccccga gctgaaggat 240
ttctacaaga gctgcatgcc cgatggctac gtgcaggagc gcaccatcac cttcgagggc 300
gatggcaatt tcaagacccg cgccgaggtg accttcgaga atggcagcgt gtacaatcgc 360
gtgaagctga aaggccaggg cttcaagaag gatggccacg tgctgggcaa gaatctggag 420
ttcaatttca cccccacta ccagtacatc tggggcgatc aggccaatca cggcctgaag 480
agcgccttca agatctgcca cgagatcacc ggcagtaagg gcgatttcat cgtggccgat 540
cacaccaga tgaatacccc catcggcggc ggccccgtgc acgtgcccgga gtaccaccac 600
atgagcaccc acgtgaagct gagcaaggat gtgaccgatc accgcgataa tatgagcctg 660
aaggagacct tgcgcgccgt ggattgccgc aagacctacc tgtga 705

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&lt;210&gt; 20

&lt;211&gt; 234

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; phiYFP-M1C1 mutant, derived from humanized version of the phiYFP-M1

&lt;400&gt; 20

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Met Ser Ser Gly Ala Gln Leu Phe His Gly Lys Ile Pro Tyr Val Val
1           5           10           15
Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
          20           25           30
Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
          35           40           45
Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
          50           55           60
Ser Trp Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65           70           75           80
Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
          85           90           95
Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
          100          105          110
Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Lys Gly Gln Gly Phe
          115          120          125
Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
          130          135          140
Pro His Tyr Gln Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145          150          155          160
Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
          165          170          175

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Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro  
 180 185 190  
 Val His Val Pro Glu Tyr His His Met Ser Thr His Val Lys Leu Ser  
 195 200 205  
 Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Leu  
 210 215 220  
 Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu  
 225 230

<210> 21  
 <211> 699  
 <212> DNA  
 <213> Artificial sequence  
 <220>  
 <223> humanized version of the S3-2 mutant  
 <400> 21

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 gtggtgaacg gccagaagtt caccatcgtg gccgacggca gcagcaagtt cccccacggc 120  
 gacttcaacg tgcacgccgt gtgcgagacc ggcaagctgc ccatgagctg gaagcccatc 180  
 tgccacctga tccagtacgg cgagcccttc ttgcgccgct accccaacgg catcagccac 240  
 ttgcgccagg agtgcttccc cgagggcgct agcatcgacc gcaccgtgcg cttcgagaac 300  
 gacggcacca tgaccagcca ccacacctac gagctggacg gcacctgcgt ggtgagccgc 360  
 atcaccgtga actgcgacgg cttccagccc gacggcccca tcatgcgcga ccagctggtg 420  
 gacatcctgc ccaacgagac ccacatgttc cccacaggcc ccaacgccgt gcgccagctg 480  
 gccttcatcg gottcaccac cgccgacggc ggccctgatga tgagccactt cgacagcaag 540  
 atgaccttca acggcagccg cgccatcaag atccccggcc ccacttcgt gaccaccatc 600  
 accaagcaga tgaaggacac cagcgacaag cgcgaccacg tgtgccagcg cgaggtgacc 660  
 tacgcccaca gcgtgccccg catcaccagc gccatctga 699

<210> 22  
 <211> 232  
 <212> PRT  
 <213> Artificial sequence  
 <220>  
 <223> humanized S3-2 mutant  
 <400> 22

Met Glu Gly Gly Pro Ala Leu Phe Gln Ser Asp Met Thr Phe Lys Ile  
 1 5 10 15



Phe Ile Asp Gly Val Val Asn Gly Gln Lys Phe Thr Ile Val Ala Asp  
 20 25 30  
 Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys  
 35 40 45  
 Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile  
 50 55 60  
 Gln Tyr Gly Glu Pro Phe Phe Ala Arg Tyr Pro Asn Gly Ile Ser His  
 65 70 75 80  
 Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Ser Ile Asp Arg Thr Val  
 85 90 95  
 Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu  
 100 105 110  
 Asp Gly Thr Cys Val Val Ser Arg Ile Thr Val Asn Cys Asp Gly Phe  
 115 120 125  
 Gln Pro Asp Gly Pro Ile Met Arg Asp Gln Leu Val Asp Ile Leu Pro  
 130 135 140  
 Asn Glu Thr His Met Phe Pro His Gly Pro Asn Ala Val Arg Gln Leu  
 145 150 155 160  
 Ala Phe Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His  
 165 170 175  
 Phe Asp Ser Lys Met Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro  
 180 185 190  
 Gly Pro His Phe Val Thr Thr Ile Thr Lys Gln Met Lys Asp Thr Ser  
 195 200 205  
 Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser  
 210 215 220  
 Val Pro Arg Ile Thr Ser Ala Ile  
 225 230